

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/055,145

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DATE: 04/16/98
TIME: 13:47:14

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This Raw Listing contains the General
Information Section and up to the first 5 pages

ENTERED

SEQUENCE LISTING

(1) General Information:

(i) APPLICANT: Weeks, Donald P.
Wang, Xiao-Zhuo
Herman, Patricia L.

(ii) TITLE OF INVENTION: "METHODS AND MATERIALS FOR MAKING AND
USING TRANSGENIC DICAMBA-DEGRADING ORGANISMS"

(iii) NUMBER OF SEQUENCES: 6

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Sheridan Ross P.C.
(B) STREET: 1700 Lincoln St., Suite 3500
(C) CITY: Denver
(D) STATE: Colorado
(E) COUNTRY: USA
(F) ZIP: 80203

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 60/042,666
(B) FILING DATE: 04-APR-1997

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 60/042,941
(B) FILING DATE: 04-APR-1997

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Crook, Wannell M.
(B) REGISTRATION NUMBER: 31,071
(C) REFERENCE/DOCKET NUMBER: 3553-18

(ix) TELECOMMUNICATION INFORMATION:

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PATENT APPLICATION US/09/055,145DATE: 04/16/98
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47 (A) TELEPHONE: (303) 863-9700
48 (B) TELEFAX: (303) 863-0223
49
50
51 (2) INFORMATION FOR SEQ ID NO:1:
52
53 (i) SEQUENCE CHARACTERISTICS:
54 (A) LENGTH: 29 amino acids
55 (B) TYPE: amino acid
56 (C) STRANDEDNESS: single
57 (D) TOPOLOGY: linear
58
59 (ii) MOLECULE TYPE: protein
60
61
62 (ix) FEATURE:
63 (A) NAME/KEY: Region
64 (B) LOCATION: 28
65 (D) OTHER INFORMATION: /note= "Best guess for Xaa = Asp or
66 Thr"
67
68 (ix) FEATURE:
69 (A) NAME/KEY: Region
70 (B) LOCATION: 29
71 (D) OTHER INFORMATION: /note= "Best guess for Xaa = Pro"
72
73
74 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
75
76 Thr Phe Val Arg Asn Ala Trp Tyr Val Ala Ala Leu Pro Glu Glu Leu
77 1 5 10 15
78
79 Ser Glu Lys Pro Leu Gly Arg Thr Ile Leu Asp Xaa Xaa
80 20 25
81
82 (2) INFORMATION FOR SEQ ID NO:2:
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84 (i) SEQUENCE CHARACTERISTICS:
85 (A) LENGTH: 20 amino acids
86 (B) TYPE: amino acid
87 (C) STRANDEDNESS: single
88 (D) TOPOLOGY: linear
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90 (ii) MOLECULE TYPE: protein
91
92
93 (ix) FEATURE:
94 (A) NAME/KEY: Region
95 (B) LOCATION: 8
96 (D) OTHER INFORMATION: /note= "Best guess for Xaa = Cys"
97
98 (ix) FEATURE:
99 (A) NAME/KEY: Region

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100         (B) LOCATION: 11
101         (D) OTHER INFORMATION: /note= "Best guess for Xaa = Cys"
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103     (ix) FEATURE:
104         (A) NAME/KEY: Region
105         (B) LOCATION: 16
106         (D) OTHER INFORMATION: /note= "Best guess for Xaa = Cys"
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108     (ix) FEATURE:
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110         (B) LOCATION: 20
111         (D) OTHER INFORMATION: /note= "Best guess for Xaa = Cys"
112
113
114     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
115
116     Thr Tyr Val Val Thr Asp Ala Xaa Ile Lys Xaa Lys Tyr Met Asp Xaa
117     1             5             10             15
118
119     Val Glu Val Xaa
120             20
121
122     (2) INFORMATION FOR SEQ ID NO:3:
123
124     (i) SEQUENCE CHARACTERISTICS:
125         (A) LENGTH: 1020 base pairs
126         (B) TYPE: nucleic acid
127         (C) STRANDEDNESS: single
128         (D) TOPOLOGY: linear
129
130     (ii) MOLECULE TYPE: cDNA
131
132
133     (ix) FEATURE:
134         (A) NAME/KEY: CDS
135         (B) LOCATION: 1..1020
136
137
138     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
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140     ATG ACC TTC GTC CGC AAT GCC TGG TAT GTG GCG GCG CTG CCC GAG GAA      48
141     Met Thr Phe Val Arg Asn Ala Trp Tyr Val Ala Ala Leu Pro Glu Glu
142     1             5             10             15
143
144     CTG TCC GAA AAG CCG CTC GGC CGG ACG ATT CTC GAC ACA CCG CTC GCG      96
145     Leu Ser Glu Lys Pro Leu Gly Arg Thr Ile Leu Asp Thr Pro Leu Ala
146             20             25             30
147
148     CTC TAC CGC CAG CCC GAC GGT GTG GTC GCG GCG CTG CTC GAC ATC TGT      144
149     Leu Tyr Arg Gln Pro Asp Gly Val Val Ala Ala Leu Leu Asp Ile Cys
150             35             40             45
151
152     CCG CAC CGC TTC GCG CCG CTG AGC GAC GGC ATC CTC GTC AAC GGC CAT      192
    
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153	Pro	His	Arg	Phe	Ala	Pro	Leu	Ser	Asp	Gly	Ile	Leu	Val	Asn	Gly	His	
154		50					55					60					
155																	
156	CTC	CAA	TGC	CCC	TAT	CAC	GGG	CTG	GAA	TTC	GAT	GGC	GGC	GGG	CAG	TGC	240
157	Leu	Gln	Cys	Pro	Tyr	His	Gly	Leu	Glu	Phe	Asp	Gly	Gly	Gly	Gln	Cys	
158	65					70				75					80		
159																	
160	GTC	CAT	AAC	CCG	CAC	GGC	AAT	GGC	GCC	CGC	CCG	GCT	TCG	CTC	AAC	GTC	288
161	Val	His	Asn	Pro	His	Gly	Asn	Gly	Ala	Arg	Pro	Ala	Ser	Leu	Asn	Val	
162					85				90					95			
163																	
164	CGC	TCC	TTC	CCG	GTG	GTG	GAG	CGC	GAC	GCG	CTG	ATC	TGG	ATC	TGG	CCC	336
165	Arg	Ser	Phe	Pro	Val	Val	Glu	Arg	Asp	Ala	Leu	Ile	Trp	Ile	Trp	Pro	
166				100				105					110				
167																	
168	GGC	GAT	CCG	GCG	CTG	GCC	GAT	CCT	GGG	GCG	ATC	CCC	GAC	TTC	GGC	TGC	384
169	Gly	Asp	Pro	Ala	Leu	Ala	Asp	Pro	Gly	Ala	Ile	Pro	Asp	Phe	Gly	Cys	
170			115				120					125					
171																	
172	CGC	GTC	GAT	CCC	GCC	TAT	CGG	ACC	GTC	GGC	GGC	TAT	GGG	CAT	GTC	GAC	432
173	Arg	Val	Asp	Pro	Ala	Tyr	Arg	Thr	Val	Gly	Gly	Tyr	Gly	His	Val	Asp	
174	130					135				140							
175																	
176	TGC	AAC	TAC	AAG	CTG	CTG	GTC	GAC	AAC	CTG	ATG	GAC	CTC	GGC	CAC	GCC	480
177	Cys	Asn	Tyr	Lys	Leu	Leu	Val	Asp	Asn	Leu	Met	Asp	Leu	Gly	His	Ala	
178	145				150				155				160				
179																	
180	CAA	TAT	GTC	CAT	CGC	GCC	AAC	GCC	CAG	ACC	GAC	GCC	TTC	GAC	CGG	CTG	528
181	Gln	Tyr	Val	His	Arg	Ala	Asn	Ala	Gln	Thr	Asp	Ala	Phe	Asp	Arg	Leu	
182				165				170					175				
183																	
184	GAG	CGC	GAG	GTG	ATC	GTC	GGC	GAC	GGT	GAG	ATA	CAG	GCG	CTG	ATG	AAG	576
185	Glu	Arg	Glu	Val	Ile	Val	Gly	Asp	Gly	Glu	Ile	Gln	Ala	Leu	Met	Lys	
186			180				185					190					
187																	
188	ATT	CCC	GGC	GGC	ACG	CCG	AGC	GTG	CTG	ATG	GCC	AAG	TTC	CTG	CGC	GGC	624
189	Ile	Pro	Gly	Gly	Thr	Pro	Ser	Val	Leu	Met	Ala	Lys	Phe	Leu	Arg	Gly	
190		195				200					205						
191																	
192	GCC	AAT	ACC	CCC	GTC	GAC	GCT	TGG	AAC	GAC	ATC	CGC	TGG	AAC	AAG	GTG	672
193	Ala	Asn	Thr	Pro	Val	Asp	Ala	Trp	Asn	Asp	Ile	Arg	Trp	Asn	Lys	Val	
194	210					215					220						
195																	
196	AGC	GCG	ATG	CTC	AAC	TTC	ATC	GCG	GTG	GCG	CCG	GAA	GGC	ACC	CCG	AAG	720
197	Ser	Ala	Met	Leu	Asn	Phe	Ile	Ala	Val	Ala	Pro	Glu	Gly	Thr	Pro	Lys	
198	225				230				235				240				
199																	
200	GAG	CAG	AGC	ATC	CAC	TCG	CGC	GGT	ACC	CAT	ATC	CTG	ACC	CCC	GAG	ACG	768
201	Glu	Gln	Ser	Ile	His	Ser	Arg	Gly	Thr	His	Ile	Leu	Thr	Pro	Glu	Thr	
202				245				250				255					
203																	
204	GAG	GCG	AGC	TGC	CAT	TAT	TTC	TTC	GGC	TCC	TCG	CGC	AAT	TTC	GGC	ATC	816
205	Glu	Ala	Ser	Cys	His	Tyr	Phe	Phe	Gly	Ser	Ser	Arg	Asn	Phe	Gly	Ile	

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206                260                265                270
207
208   GAC GAT CCG GAG ATG GAC GGC GTG CTG CGC AGC TGG CAG GCT CAG GCG      864
209   Asp Asp Pro Glu Met Asp Gly Val Leu Arg Ser Trp Gln Ala Gln Ala
210                275                280                285
211
212   CTG GTC AAG GAG GAC AAG GTC GTC GTC GAG GCG ATC GAG CGC CGC CGC      912
213   Leu Val Lys Glu Asp Lys Val Val Val Glu Ala Ile Glu Arg Arg Arg
214                290                295                300
215
216   GCC TAT GTC GAG GCG AAT GGC ATC CGC CCG GCG ATG CTG TCG TGC GAC      960
217   Ala Tyr Val Glu Ala Asn Gly Ile Arg Pro Ala Met Leu Ser Cys Asp
218   305                310                315                320
219
220   GAA GCC GCA GTC CGT GTC AGC CGC GAG ATC GAG AAG CTT GAG CAG CTC      1008
221   Glu Ala Ala Val Arg Val Ser Arg Glu Ile Glu Lys Leu Glu Gln Leu
222                325                330                335
223
224   GAA GCC GCC TGA
225   Glu Ala Ala *
226                340
227
228
229   (2) INFORMATION FOR SEQ ID NO:4:
230
231       (i) SEQUENCE CHARACTERISTICS:
232           (A) LENGTH: 339 amino acids
233           (B) TYPE: amino acid
234           (D) TOPOLOGY: linear
235
236       (ii) MOLECULE TYPE: protein
237
238       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
239
240   Met Thr Phe Val Arg Asn Ala Trp Tyr Val Ala Ala Leu Pro Glu Glu
241       1                5                10                15
242
243   Leu Ser Glu Lys Pro Leu Gly Arg Thr Ile Leu Asp Thr Pro Leu Ala
244       20                25                30
245
246   Leu Tyr Arg Gln Pro Asp Gly Val Val Ala Ala Leu Leu Asp Ile Cys
247       35                40                45
248
249   Pro His Arg Phe Ala Pro Leu Ser Asp Gly Ile Leu Val Asn Gly His
250       50                55                60
251
252   Leu Gln Cys Pro Tyr His Gly Leu Glu Phe Asp Gly Gly Gly Gln Cys
253       65                70                75                80
254
255   Val His Asn Pro His Gly Asn Gly Ala Arg Pro Ala Ser Leu Asn Val
256       85                90                95
257
258   Arg Ser Phe Pro Val Val Glu Arg Asp Ala Leu Ile Trp Ile Trp Pro

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SEQUENCE VERIFICATION REPORT
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